

FIG. 1A

GAATTCTCTGGACTGAGGCTCCAGTTCTGGCCTTTGGGG

TTCAAGATCACTGGGACCAGGCCGTGATCTCTATGCCCCGAGTCTCAACCCTCAACTGTC

ACCCCAAGGCACTTGGGACGTCCTGGACAGACCGAGTCCCGGGAAGCCCCAGCACTGCC

GCTGCCACACTGCCCTGAGCCCAAATGGGGGAGTGAGAGGCCA TAG CTG TCT GGC

S1		S5		S10		S15
Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu						
ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCA CTG GTG CTC						
216		225		234		243 252

	S20		S25		S29	1
Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu						
CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG						
261	270		279		288	297

	5		10		15
Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro					
GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC					
306	315		324		333 342

	20		25		30
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr					
CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC					
351	360		369		378 387

	35		40		45
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro					
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG					
396	405		414		423 432

	50		55		60
Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr					
GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC					
441	450		459		468 477

	65		70		75
Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys					
GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC					
486	495		504		513 522

	80		85		90
Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp					
CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC					
531	540		549		558 567

FIG. 1B

Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr
CGG	GAC	ACC	GTG	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT
576			585			594			603			612		
Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu
TGG	AGT	GAA	AAC	CTT	TTC	CAG	TGC	TTC	AAT	TGC	AGC	CTC	TGC	CTC
621			630			639			648			657		
Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val
AAT	GGG	ACC	GTG	CAC	CTC	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG
666			675			684			693			702		
Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val
TGC	ACC	TGC	CAT	GCA	GGT	TTC	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC
711			720			729			738			747		
Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	Lys	Leu	Cys
TCC	TGT	AGT	AAC	TGT	AAG	AAA	AGC	CTG	GAG	TGC	ACG	AAG	TTG	TGC
756			765			774			783			792		
Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser	Gly	Thr
CTA	CCC	CAG	ATT	GAG	AAT	GTT	AAG	GGC	ACT	GAG	GAC	TCA	GGC	ACC
801			810			819			828			837		
Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu	Leu
ACA	GTG	CTG	TTG	CCC	CTG	GTC	ATT	TTC	TTT	GGT	CTT	TGC	CTT	TTA
846			855			864			873			882		
Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys
TCC	CTC	CTC	TTC	ATT	GGT	TTA	ATG	TAT	CGC	TAC	CAA	CGG	TGG	AAG
891			900			909			918			927		
Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys
TCC	AAG	CTC	TAC	TCC	ATT	GTT	TGT	GGG	AAA	TCG	ACA	CCT	GAA	AAA
936			945			954			963			972		
Glu	Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn
GAG	GGG	GAG	CTT	GAA	GGA	ACT	ACT	ACT	AAG	CCC	CTG	GCC	CCA	AAC
981			990			999			1008			1017		

FIG. 1C

Pro	Ser	Phe	245	Ser	Pro	Thr	Pro	Gly	250	Phe	Thr	Pro	Thr	Leu	Gly	Phe	255
CCA	AGC	TTC	AGT	CCC	ACT	CCA	GGC	TTC	ACC	CCC	ACC	CTG	GGC	TTC			
1026			1035			1044			1053			1062					
Ser	Pro	Val	260	Pro	Ser	Ser	Thr	Phe	265	Thr	Ser	Ser	Ser	Thr	Tyr	Thr	270
AGT	CCC	GTG	CCC	AGT	TCC	ACC	TTC	ACC	TCC	AGC	TCC	ACC	TAT	ACC			
1071			1080			1089			1098			1107					
Pro	Gly	Asp	275	Cys	Pro	Asn	Phe	Ala	280	Ala	Pro	Arg	Arg	Glu	Val	Ala	285
CCC	GGT	GAC	TGT	CCC	AAC	TTT	GCG	GCT	CCC	CGC	AGA	GAG	GTG	GCA			
1116			1125			1134			1143			1152					
Pro	Pro	Tyr	290	Gln	Gly	Ala	Asp	Pro	295	Ile	Leu	Ala	Thr	Ala	Leu	Ala	300
CCA	CCC	TAT	CAG	GGG	GCT	GAC	CCC	ATC	CTT	GCG	ACA	GCC	CTC	GCC			
1161			1170			1179			1188			1197					
Ser	Asp	Pro	305	Ile	Pro	Asn	Pro	Leu	310	Gln	Lys	Trp	Glu	Asp	Ser	Ala	315
TCC	GAC	CCC	ATC	CCC	AAC	CCC	CTT	CAG	AAG	TGG	GAG	GAC	AGC	GCC			
1206			1215			1224			1233			1242					
His	Lys	Pro	320	Gln	Ser	Leu	Asp	Thr	325	Asp	Asp	Pro	Ala	Thr	Leu	Tyr	330
CAC	AAG	CCA	CAG	AGC	CTA	GAC	ACT	GAT	GAC	CCC	GCG	ACG	CTG	TAC			
1251			1260			1269			1278			1287					
Ala	Val	Val	335	Glu	Asn	Val	Pro	Pro	340	Leu	Arg	Trp					
GCC	GTG	GTG	GAG	AAC	GTG	CCC	CCG	TTG	CGC	TGG	AA	GGAATTC					
1296			1305			1314			1323			1332					

FIG. 2

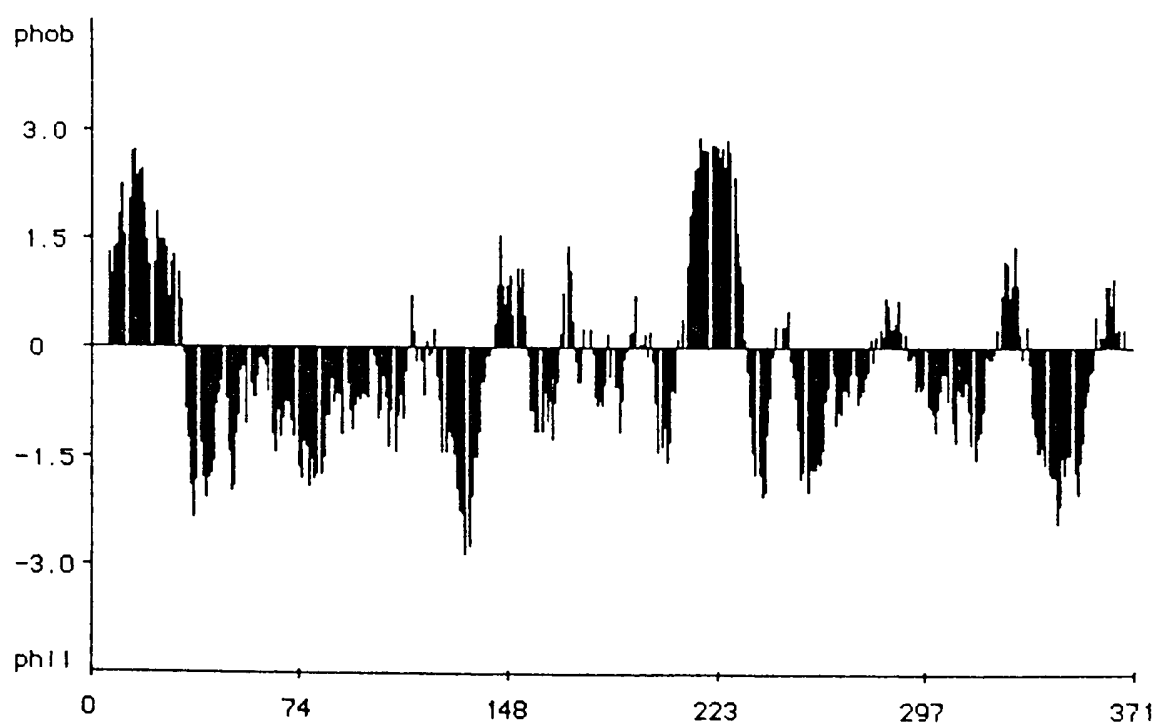


FIG. 3A

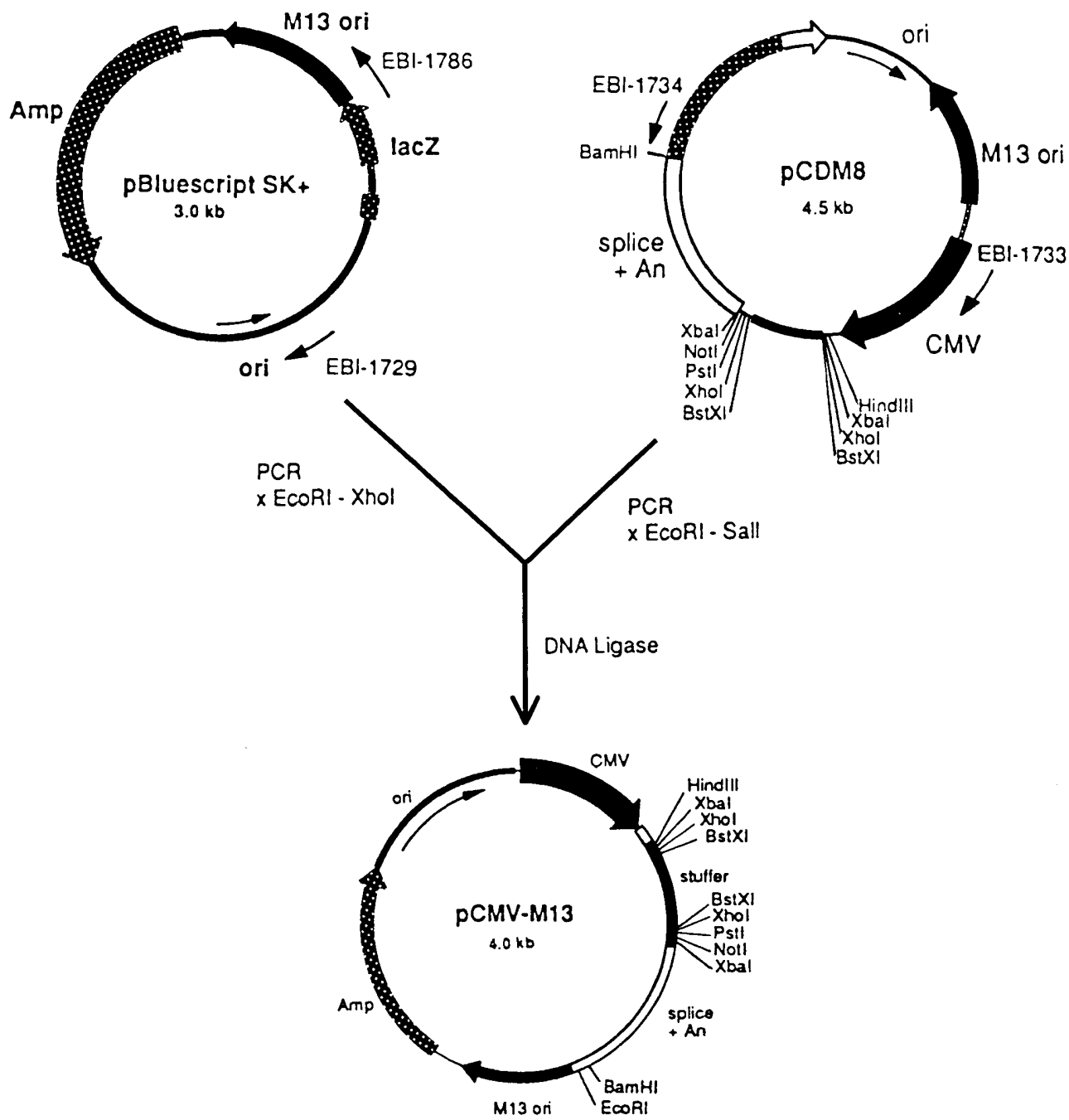


FIG. 3B

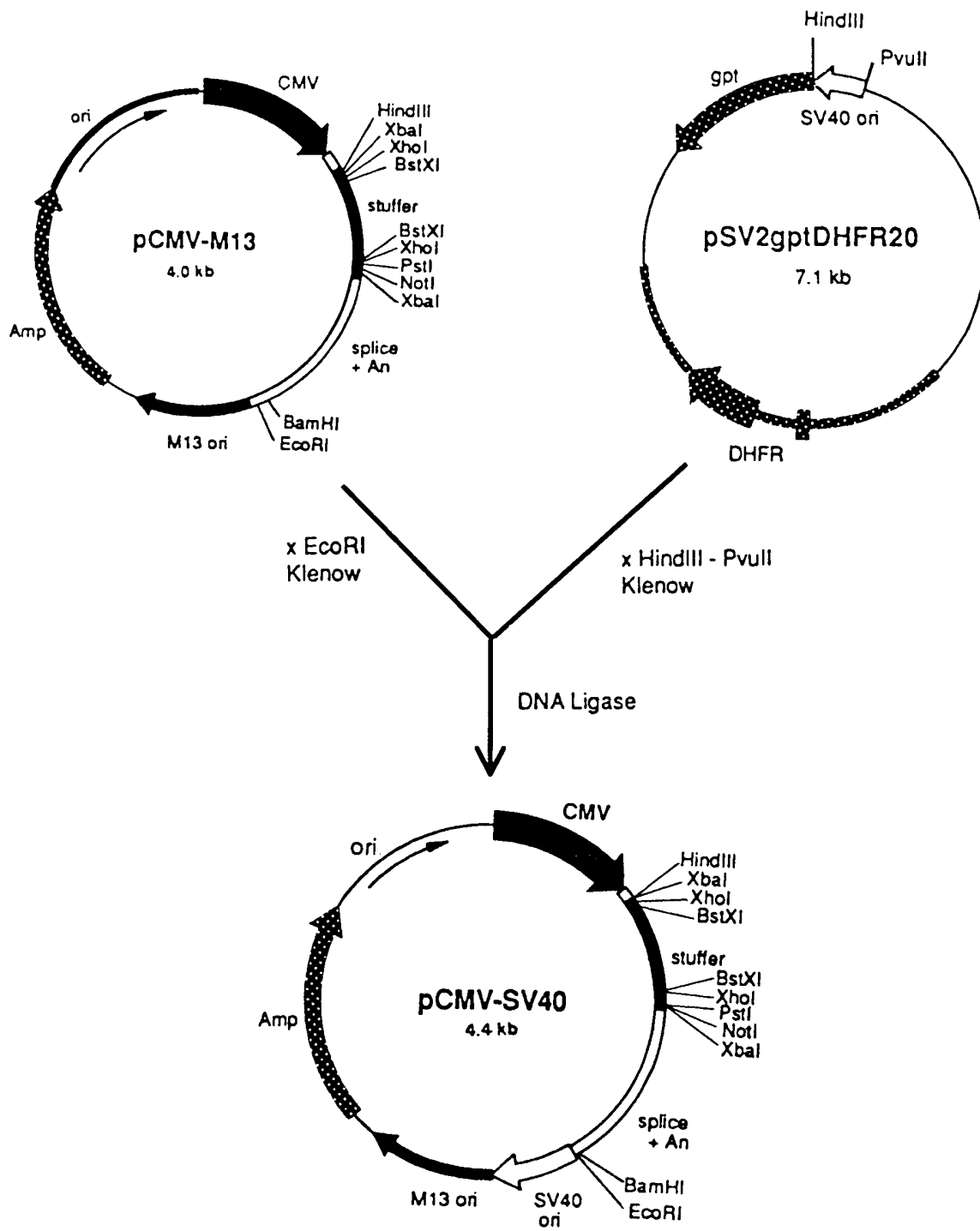


FIG. 4A

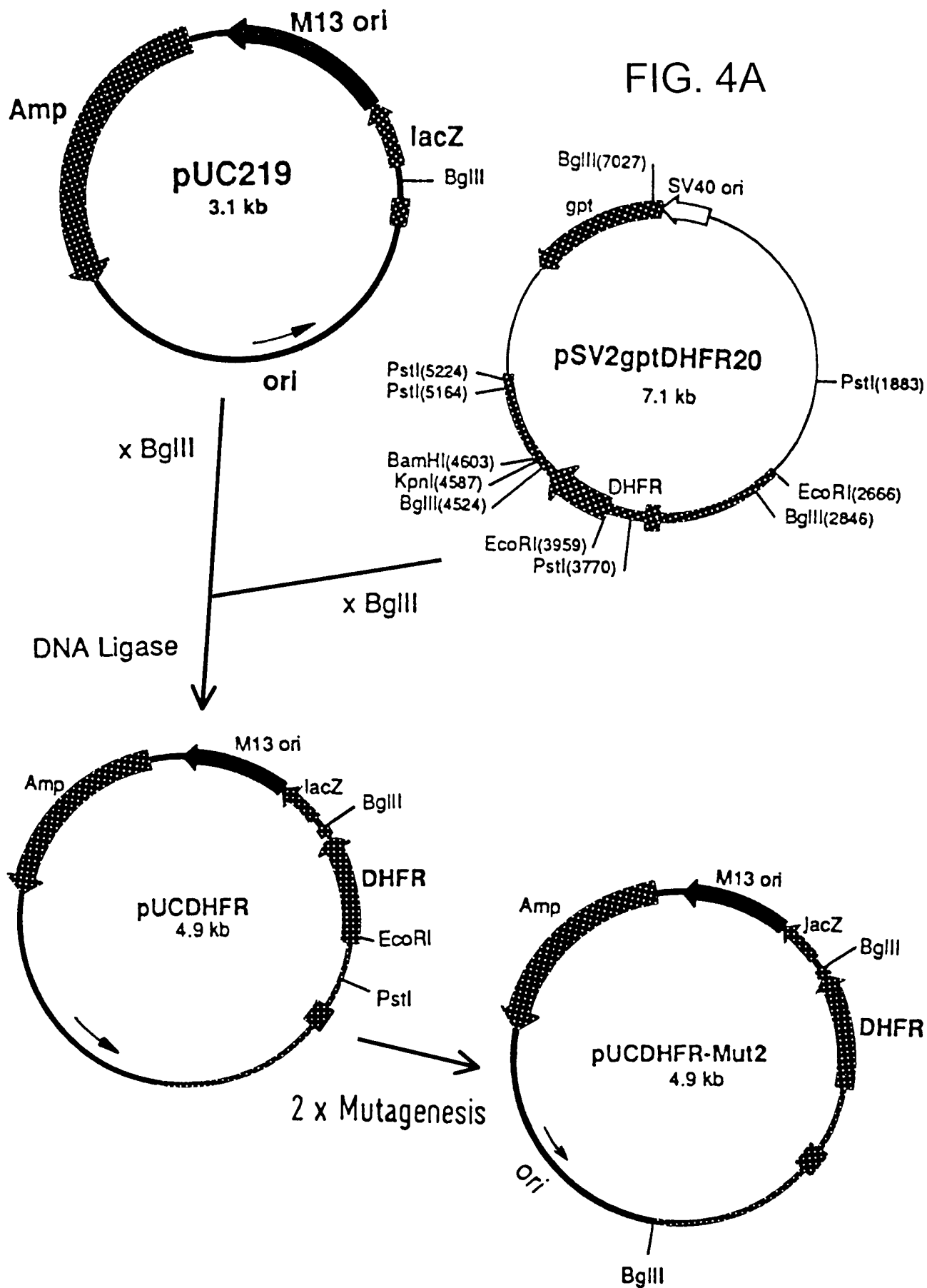
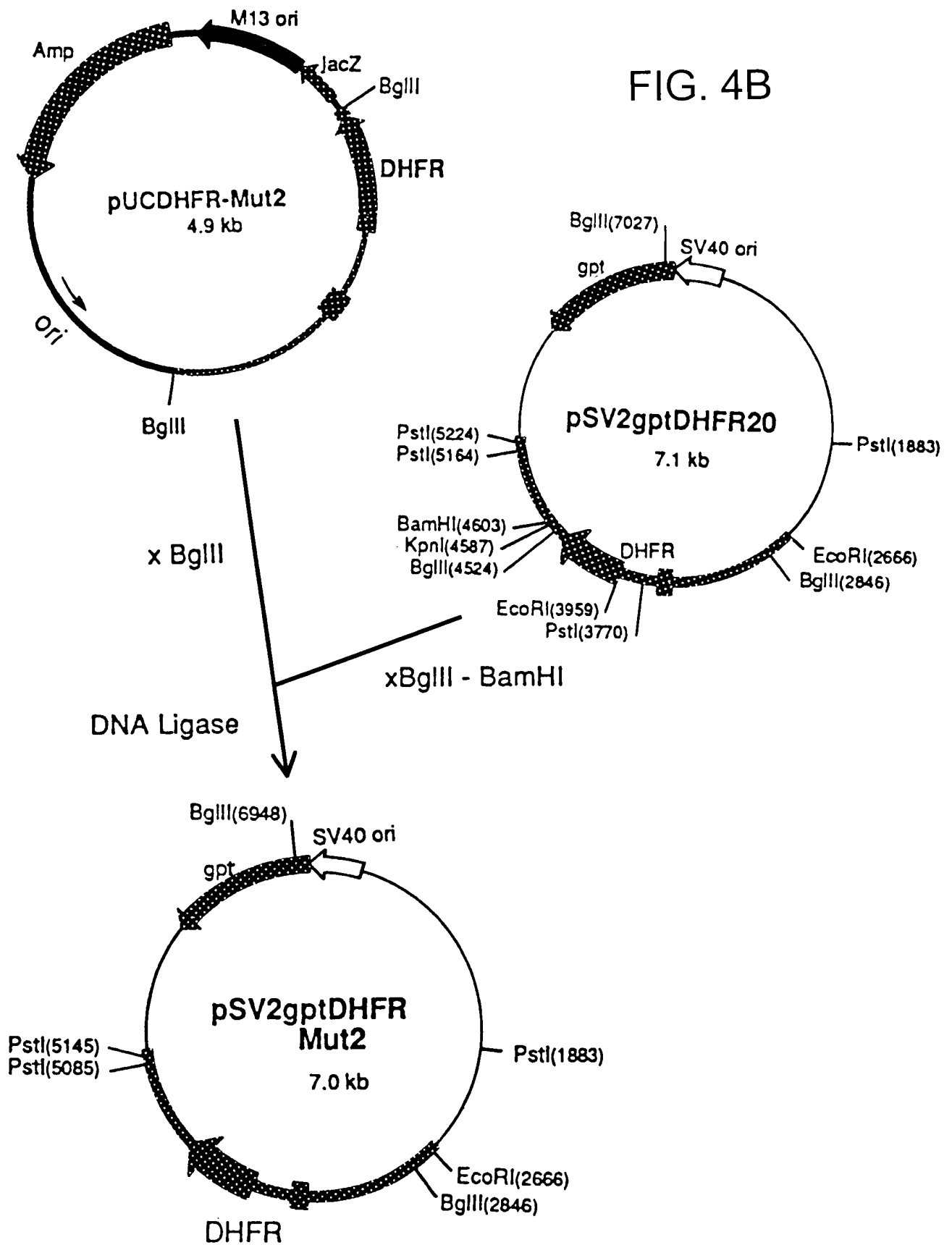


FIG. 4B



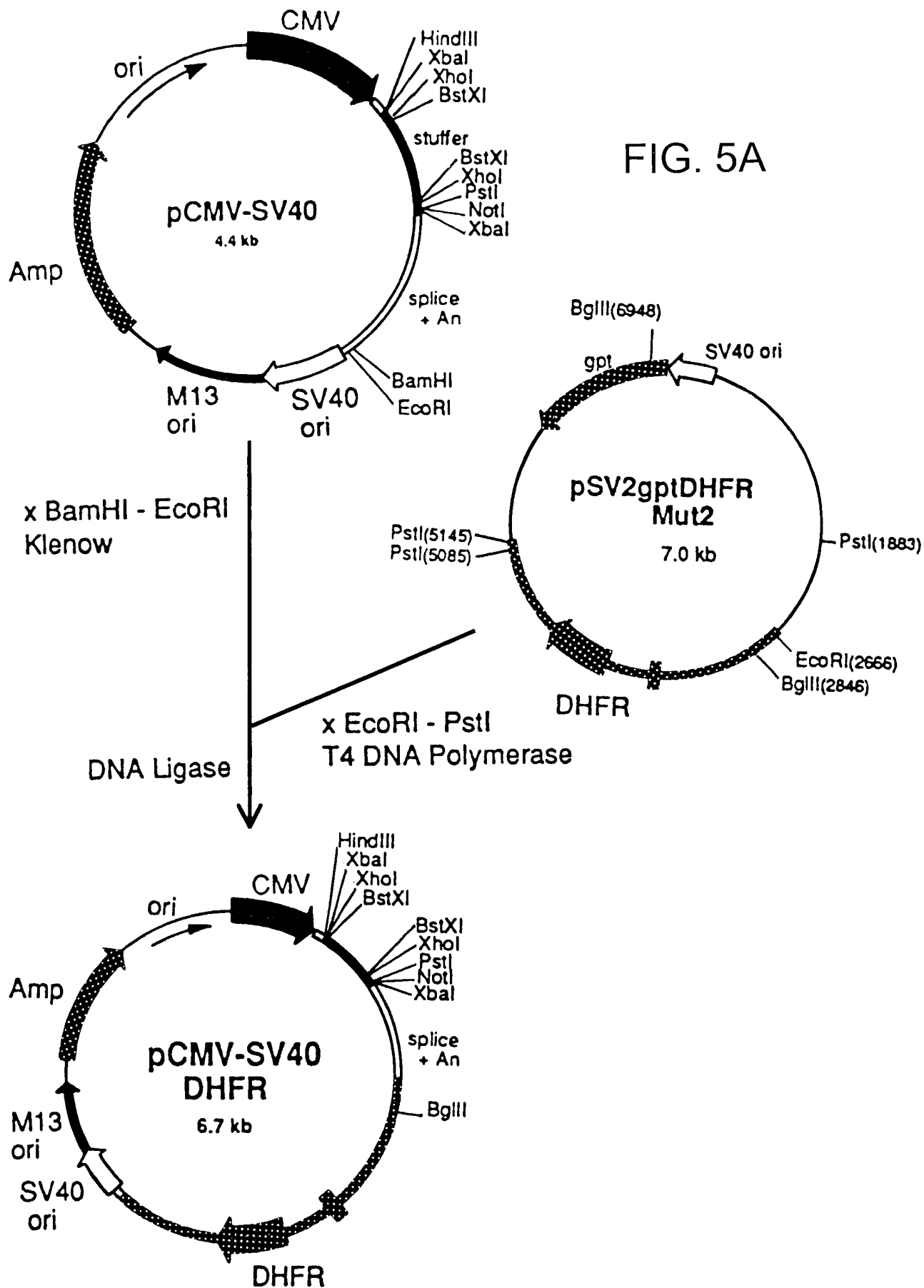


FIG. 5B

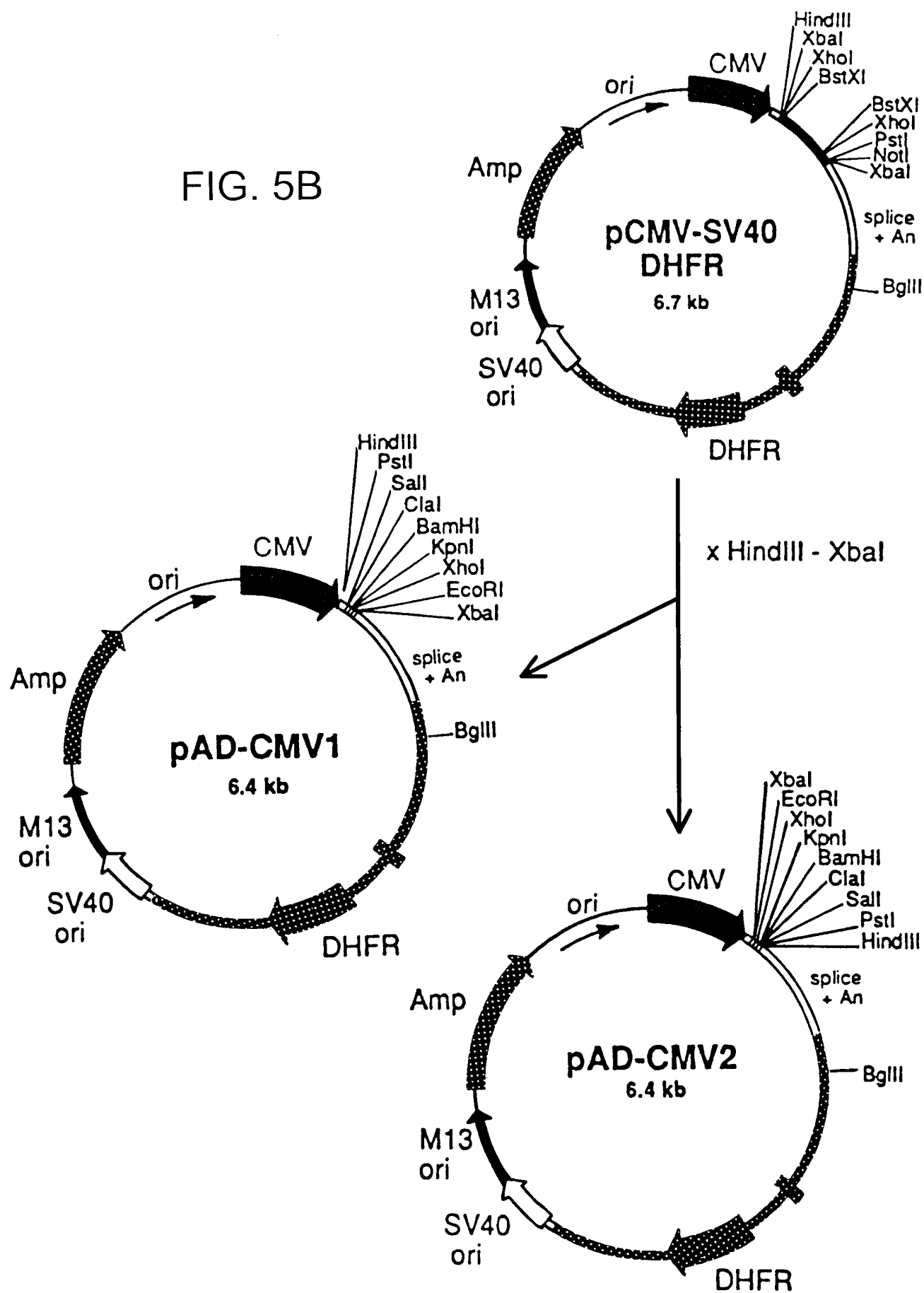


FIG. 6A

pAD-CMV1 : 6414 bp

TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT TAGTTCATAG	60
CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCCTG GCTGACCGCC	120
CAACGACCCC CGCCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA CGCCAATAGG	180
GACTTTCCAT TGACGTCAAT GGGTGGAGTA TTTACGGTAA ACTGCCCCACT TGGCAGTACA	240
TCAAGTGTAT CATATGCCAA GTACGCCCCC TATTGACGTC AATGACGGTA AATGGCCCCG	300
CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTTGGCAGT ACATCTACGT	360
ATTAGTCATC GCTATTACCA TGGTGATGCG GTTTTGGCAG TACATCAATG GCGTGAGATA	420
GCGGTTTGAC TCACGGGGAT TTCCAAGTCT CCACCCCAT TACGTCAATG GGAGTTTGTT	480
TTGGCACCAA AATCAACGGG ACTTTCCAAA ATGTCGTAAC AACTCCGCCC CATTGACGCA	540
AATGGGCGGT AGGCGTGTAC GGTGGGAGGT CTATATAAGC AGAGCTCTCT GGCTAACTAG	600
AGAACCCACT GCTTAACTGG CTTATCGAAA TTAATACGAC TCACTATAGG GAGACCCAAG	660
CTTCTGCAGG TCGACATCGA TGGATCCGGT ACCTCGAGCG CGAATTCTCT AGAGGATCTT	720
TGTGAAGGAA CCTTACTTCT GTGGTGTGAC ATAATTGGAC AACTACCTA CAGAGATTTA	780
AAGCTCTAAG GTAAATATAA AATTTTTAAG TGTATAATGT GTTAACTAC TGATTCTAAT	840
TGTTTGTGTA TTTTAGATTC CAACCTATGG AACTGATGAA TGGGAGCAGT GGTGGAATGC	900
CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA TCTAGTGATG ATGAGGCTAC	960
TGCTGACTCT CAACATTCTA CTCCTCCAAA AAAGAAGAGA AAGGTAGAAG ACCCCAAGGA	1020
CTTTCCTTCA GAATTGCTAA GTTTTTTGAG TCATGCTGTG TTTAGTAATA GAACTCTTGC	1080
TTGCTTTGCT ATTTACACCA CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA	1140
AAAATATTTG ATGTATAGTG CCTTGACTAG AGATCATAAT CAGCCATACC ACATTTGTAG	1200
AGGTTTTACT TGCTTTAAAA AACCTCCAC ACCTCCCCCT GAACCTGAAA CATAAAATGA	1260
ATGCAATTGT TGTTGTAAAC TTGTTTATTG CAGCTTATAA TGGTTACAAA TAAAGCAATA	1320
GCATCACAAA TTTCACAAAT AAAGCATTTT TTCACTGCA TTCTAGTTGT GGTGTGTCCA	1380
AACTCATCAA TGTATCTTAT CATGTCTGGA TCAATTCTGA GAACTAGCC TTAAAGACAG	1440

FIG. 6B

ACAGCTTTGT TCTAGTCAGC CAGGCAAGCA TATGTAAATA AAGTTCCTCA GGGAAGTCTGAG	1500
GTAAAAAGAT GTATCCTGGA CCTGCCAGAC CTGGCCATTC ACGTAAACAG AAGATTCCGC	1560
CTCAAGTTCC GGTTAACAAC AGGAGGCAAC GAGATCTCAA ATCTATTACT TCTAATCGGG	1620
TAATTAAAAAC CTTTCAACTA AAACACGGAC CCACGGATGT CACCCACTTT TCCTTCCCCG	1680
GCTCCGCCCT TCTCAGTACT CCCCACCATT AGGCTCGCTA CTCCACCTCC ACTTCCGGGC	1740
GCGACACCCA CGTGCCCTCT CCCACCCGAC GCTAACCCCG CCCCTGCCCCG TCTGACCCCG	1800
CCCACCACCT GGCCCCGCCC CGTTGAGGAC AGAAGAAACC CCGGGCAGCC GCAGCCAAGG	1860
CGGACGGGTA GACGCTGGGG GCGCTGAGGA GTCGTCTCT ACCTTCTCTG CTGGCTCGGT	1920
GGGGGACGCG GTGGATCTCA GGCTTCCGGA AGACTGGAAG AACC GGCTCA GAACCGCTTG	1980
TCTCCGCGGG GCTTGGGCGG CGGAAGAATG GCCGCTAGAC GCGGACTTGG TCGGAGGCAT	2040
CGCAGGATGC AGAAGAGCAA GCCCGCCGGG AGCGCGCGGC TGTACTACCC CGCGCCTGGA	2100
GCGGCCACGC CGGACTGGGC GGGGCCGGCC TGGTGGAGGC GGAGTCTGAC CTCGTGGAGG	2160
CGGGGCCTCT GATGTTCAAA TAGGATGCTA GGCTTGTTGA GCGTGGCCT CCGATTACACA	2220
AGTGGGAAGC AGCGCCGGGC GACTGCAATT TCGCGCCAAA CTTGGGGGAA GCACAGCGTA	2280
CAGGCTGCCT AGGTGATCGC TGCTGCTGTC ATGGTTTCGAC CGCTGAACTG CATCGTCGCC	2340
GTGTCCCAGA ATATGGGCAT CGGCAAGAAC GGAGACCTTC CCTGGCCAAT GCTCAGGTAC	2400
TGGCTGGATT GGGTTAGGGA AACCGAGGCG GTTCGCTGAA TCGGGTCGAG CACTTGGCGG	2460
AGACGCGCGG GCCAACTACT TAGGGACAGT CATGAGGGGT AGGCCCGCCG GCTGCTGCCC	2520
TTGCCCATGC CCGCGGTGAT CCCCATGCTG TGCCAGCCTT TGCCCAGAGG CGCTCTAGCT	2580
GGGAGCAAAG TCCGGTCACT GGGCAGCACC ACCCCCCGGA CTTGCATGGG TAGCCGCTGA	2640
GATGGAGCCT GAGCACACGT GACAGGGTCC CTGTTAACGC AGTGTTTCTC TAACTTTCAG	2700
GAACGAGTTC AAGTACTTCC AAAGAATGAC CACCACCTCC TCAGTGGAAG GTAAACAGAA	2760
CCTGGTGATT ATGGGCCGGA AAACCTGGTT CTCCATTCTT GAGAAGAATC GACCTTTAAA	2820
GGACAGAATT AATATAGTTC TCAGTAGAGA GCTCAAGGAA CCACCACAAG GAGCTCATTT	2880
TCTTGCCAAA AGTCTGGACC ATGCCTTAAA ACTTATTGAA CAACCAGAGT TAGCAGATAA	2940
AGTGGACATG GTTTGGATAG TTGGAGGCAG TTCCGTTTAC AAGGAAGCCA TGAATCAGCC	3000

FIG. 6C

AGGCCATCTC	AGACTCTTTG	TGACAAGGAT	CATGCAGGAA	TTTGAAAGTG	ACACGTTCTT	3060
CCCAGAAATT	GATTTGGAGA	AATATAAACT	TCTCCCAGAG	TACCCAGGGG	TCCTTTCTGA	3120
AGTCCAGGAG	GAAAAAGGCA	TCAAGTATAA	ATTTGAAGTC	TATGAGAAGA	AAGGCTAACA	3180
GAAAGATACT	TGCTGATTGA	CTTCAAGTTC	TACTGCTTTC	CTCCTAAAAT	TATGCATTTT	3240
TACAAGACCA	TGGGACTTGT	GTTGGCTTTA	GATCCTGTGC	ATCCTGGGCA	ACTGTTGTAC	3300
TCTAAGCCAC	TCCCCAAAGT	CATGCCCCAG	CCCCTGTATA	ATTCTAAACA	ATTAGAATTA	3360
TTTTCATTTT	CATTAGTCTA	ACCAGGTTAT	ATTAAATATA	CTTTAAGAAA	CACCATTTCG	3420
CATAAAGTTC	TCAATGCCCC	TCCCATGCAG	CCTCAAGTGG	CTCCCCAGCA	GATGCATAGG	3480
GTAGTGTGTG	TACAAGAGAC	CCCAAAGACA	TAGAGCCCCT	GAGAGCATGA	GCTGATATGG	3540
GGGCTCATAG	AGATAGGAGC	TAGATGAATA	AGTACAAAGG	GCAGAAATGG	GTTTTAACCA	3600
GCAGAGCTAG	AACTCAGACT	TTAAAGAAAA	TTAGATCAAA	GTAGAGACTG	AATTATTCTG	3660
CACATCAGAC	TCTGAGCAGA	GTTCTGTTCA	CTCAGACAGA	AAATGGGTAA	ATTGAGAGCT	3720
GGCTCCATTG	TGCTCCTTAG	AGATGGGAGC	AGGTGGAGGA	TTATATAAGG	TCTGGAACAT	3780
TTAACTTCTC	CGTTTCTCAT	CTTCAGTGAG	ATTCCAAGGG	ATACTACAAT	TCTGTGGAAT	3840
GTGTGTCACT	TAGGGTGTGG	AAAGTCCCCA	GGCTCCCCAG	CAGGCAGAAG	TATGCAAAGC	3900
ATGCATCTCA	ATTAGTCAGC	AACCAGGTGT	GGAAAGTCCC	CAGGCTCCCC	AGCAGGCAGA	3960
AGTATGCAAA	GCATGCATCT	CAATTAGTCA	GCAACCATAG	TCCCGCCCCT	AACTCCGCCC	4020
ATCCCGCCCC	TAATCCGCC	CAGTTCCGCC	CATTCTCCGC	CCCATGGCTG	ACTAATTTTT	4080
TTTATTTATG	CAGAGGCCGA	GGCGCCTCTG	AGCTATTCCA	GAAGTAGTGA	GGAGGCTTTT	4140
TTGGAGGCCT	AGGCTTTTGC	AAAAAAGCTA	ATTCAGCCTG	AATGGCGAAT	GGGACGCGCC	4200
CTGTAGCGGC	GCATTAAGCG	CGGCGGGTGT	GGTGGTTACG	CGCAGCGTGA	CCGCTACACT	4260
TGCCAGCGCC	CTAGCGCCCG	CTCCTTTCGC	TTTCTTCCCT	TCCTTTCTCG	CCACGTTTCG	4320
CGGCTTTCCC	CGTCAAGCTC	TAAATCGGGG	GCTCCCTTTA	GGGTTCCGAT	TTAGTGCTTT	4380
ACGGCACCTC	GACCCCAAAA	ACTTGATTAG	GGTGATGGTT	CACGTAGTGG	GCCATCGCCC	4440
TGATAGACGG	TTTTTCGCCC	TTTGACGTTG	GAGTCCACGT	TCTTTAATAG	TGGACTCTTG	4500
TTCCAAACTG	GAACAACACT	CAACCCTATC	TCGGTCTATT	CTTTTGATTT	ATAAGGGATT	4560

FIG. 6D

TTGCCGATTT CGGCCTATTG GTTAAAAAAT GAGCTGATTT AACAAAAATT TAACGCGAAT	4620
TTTAACAAAA TATTAACGTT TACAATTTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA	4680
ACCCCTATTT GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA	4740
CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT	4800
GTCGCCCTTA TTCCCTTTTT TCGGCATTT TGCCTTCCTG TTTTGTCTCA CCCAGAAACG	4860
CTGGTGAAAG TAAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG	4920
GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTGCCCCG AAGAACGTTT TCCAATGATG	4980
AGCACTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC CGGGCAAGAG	5040
CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA	5100
GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG	5160
AGTGATAACA CTGCGGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC	5220
GCTTTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG	5280
AATGAAGCCA TACCAAACGA CGAGCGTGAC ACCACGATGC CTGTAGCAAT GGCAACAACG	5340
TTGCGCAAAC TATTAAGTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC	5400
TGGATGGAGG' CGGATAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG	5460
TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG	5520
GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT	5580
ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA	5640
CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAAACTTCA TTTTAAATT	5700
AAAAGGATCT AGGTGAAGAT CCTTTTTGAT AATCTCATGA CCAAATCCC TTAACGTGAG	5760
TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT	5820
TTTTTTCTGC GCGTAATCTG CTGCTTGCAA AAAAAAAC CACCGCTACC AGCGGTGGTT	5880
TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG	5940
CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT	6000
GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC	6060
GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG	6120

FIG. 6E

TCGGGCTGAA	CGGGGGGTTC	GTGCACACAG	CCCAGCTTGG	AGCGAACGAC	CTACACCGAA	6180
CTGAGATACC	TACAGCGTGA	GCATTGAGAA	AGCGCCACGC	TTCCCGAAGG	GAGAAAGGCG	6240
GACAGGTATC	CGGTAAGCGG	CAGGGTCGGA	ACAGGAGAGC	GCACGAGGGA	GCTTCCAGGG	6300
GGAAACGCCT	GGTATCTTTA	TAGTCCTGTC	GGGTTTCGCC	ACCTCTGACT	TGAGCGTCGA	6360
TTTTTGTGAT	GCTCGTCAGG	GGGGCGGAGC	CTATGGAAAA	ACGCCAGCAA	CGCC	

FIG. 7A

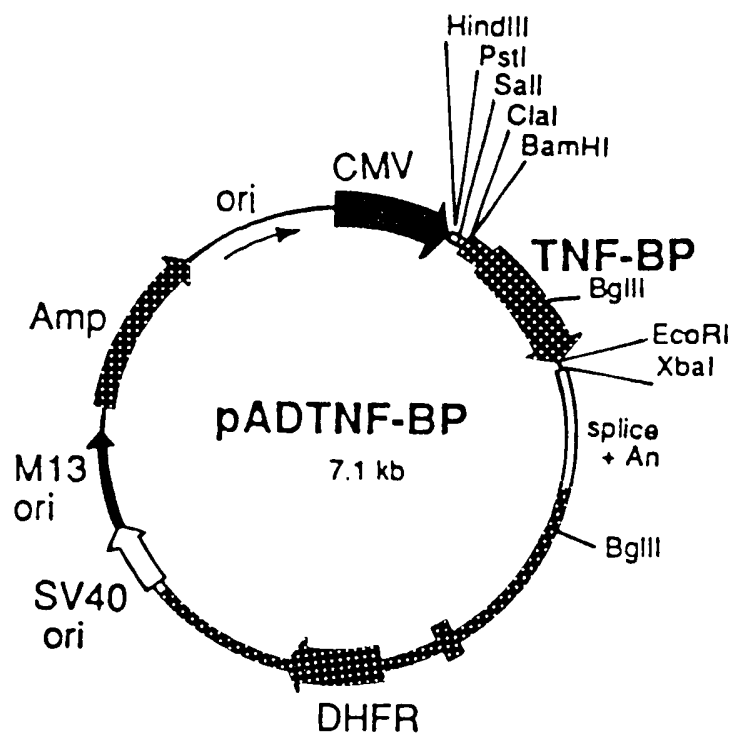


FIG. 7B

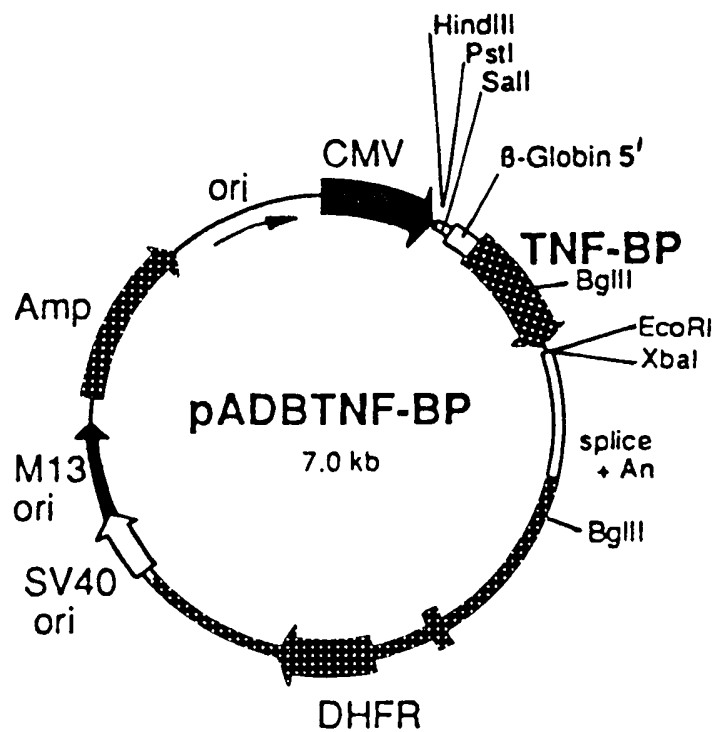


FIG. 7C

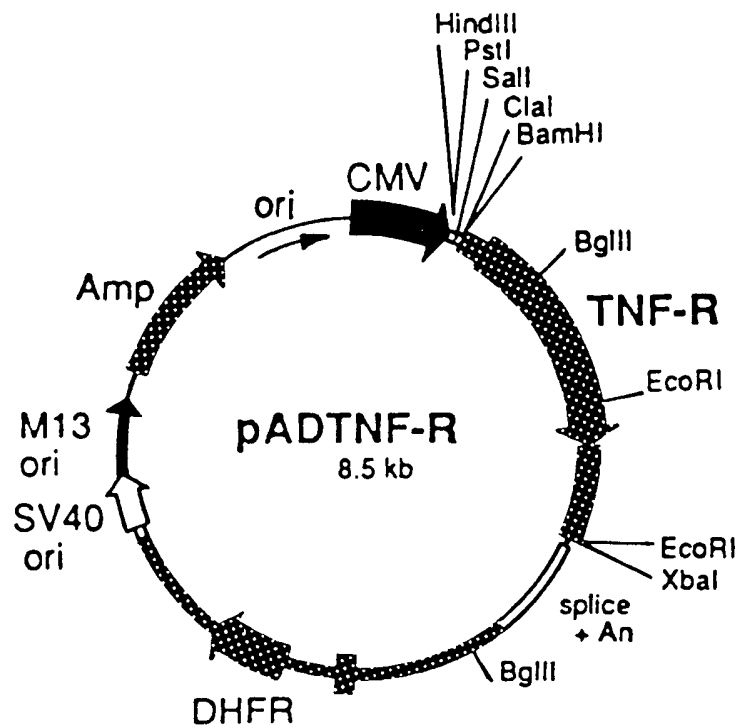


FIG. 7D

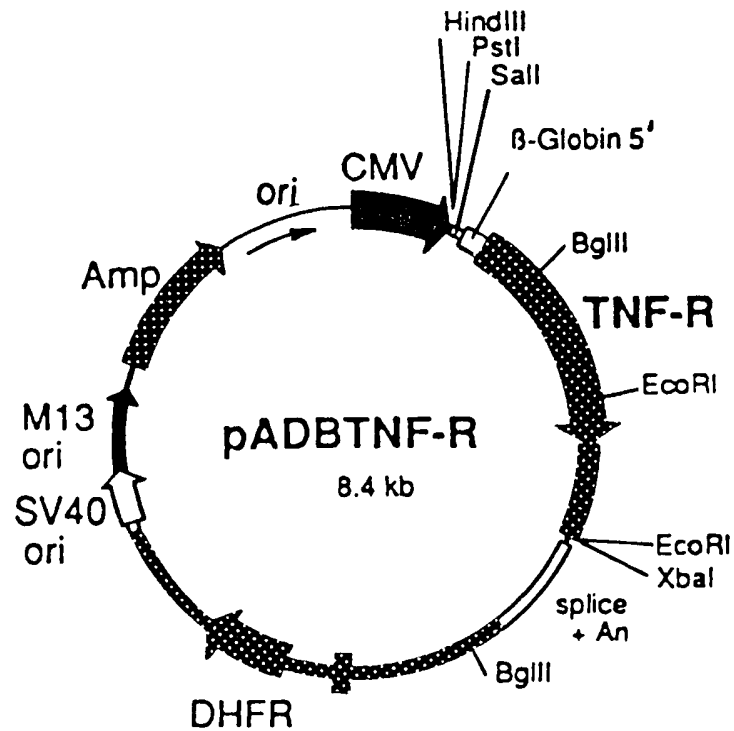


FIG. 8A

raTNF-R

GAATTCCTTT TCTCCGAGTT TTCTGAACTC TGGCTCATGA TCGGGCTTAC TGGATACGAG	60
AATCCTGGAG, GACCGTACCC TGATTTCCAT CTACCTCTGA CTTTGAGCCT TTCTAACCCG	120
GGGCTCACGC TGCCAACACC CGGGCCACCT GGTCCGATCG TCTTACTTCA TTCACCAGCG	180
TTGCCAATTG CTGCCCTGTC CCCAGCCCCA ATGGGGGAGT GAGAGAGGCC ACTGCCGGCC	240
GGAC	
245/1	275/11
ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CTG TCA CTG GTG CTC CTG GCT CTG CTG ATG	
Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu Leu Ala Leu Leu Met	
305/21	335/31
GGG ATA CAC CCA TCA GGG GTC ACC GGA CTG GTT CCT TCT CTT GGT GAC CGG GAG AAG AGG	
Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro Ser Leu Gly Asp Arg Glu Lys Arg	
365/41	395/51
GAT AAT TTG TGT CCC CAG GGA AAG TAT GCC CAT CCA AAG AAT AAT TCC ATC TGC TGC ACC	
Asp Asn Leu Cys Pro Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr	
425/61	455/71
AAG TGC CAC AAA GGA ACC TAC TTG GTG AGT GAC TGT CCA AGC CCA GGG CAG GAA ACA GTC	
Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val	
485/81	515/91
TGC GAG CTC TCT CAT AAA GGC ACC TTT ACA GCT TCG CAG AAC CAC GTC AGA CAG TGT CTC	
Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val Arg Gln Cys Leu	
545/101	575/111
AGT TGC AAG ACA TGT CGG AAA GAA ATG TTC CAG GTG GAG ATT TCT CCT TGC AAA GCT GAC	
Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp	
605/121	635/131
ATG GAC ACC GTG TGT GGC TGC AAG AAG AAC CAA TTC CAG CGC TAC CTG AGT GAG ACG CAT	
Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His	
665/141	695/151
TTC CAG TGT GTG GAC TGC AGC CCC TGC TTC AAT GGC ACC GTG ACA ATC CCC TGT AAG GAG	
Phe Gln Cys Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu	
725/161	755/171
AAA CAG AAC ACC GTG TGT AAC TGC CAC GCA GGA TTC TTT CTA AGC GGA AAT GAG TGC ACC	
Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr	
785/181	815/191
CCT TGC AGC CAC TGC AAG AAA AAT CAG GAA TGT ATG AAG CTG TGC CTA CCT CCA GTT GCA	
Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met Lys Leu Cys Leu Pro Pro Val Ala	
845/201	875/211
AAT GTC ACA AAC CCC CAG GAC TCA GGT ACT GCC GTG CTG TTG CCT CTG GTT ATC TTC CTA	
Asn Val Thr Asn Pro Gln Asp Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu	
905/221	935/231
GGT CTT TGC CTT TTA TTC TTT ATC TGC ATC AGT CTA CTG TGC CGA TAT CCC CAG TGG AGG	
Gly Leu Cys Leu Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg	
965/241	995/251
CCC AGG GTC TAC TCC ATC ATT TGT AGG GAT TCA GCT CCT GTC AAA GAG GTG GAG GGT GAA	
Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu Val Glu Gly Glu	
1025/261	1055/271
GGA ATT GTT ACT AAG CCC CTA ACT CCA GCC TCT ATT CCA GCC TTC AGC CCC AAC CCC GGC	
Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly	
1085/281	1115/291
TTC AAC CCC ACT CTG GGC TTC AGC ACC ACC CCA CGC TTC AGT CAT CCT GTC TCC AGT ACC	
Phe Asn Pro Thr Leu Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr	
1145/301	1175/311
CCC ATC AGC CCC GTC TTC GGT CCT AGT AAC TGG CAC AAC TTC GTG CCA CCT GTA AGA GAG	
Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu	
1205/321	1235/331
GTG GTC CCA ACC CAG GGT GCT GAC CCT CTC CTC TAC GGA TCC CTC AAC CCT GTG CCA ATC	
Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile	

FIG. 8B

1265/341

CCC GCC CCT GTT CGG AAA TGG GAA GAC GTC GTC GCG GCC CAG CCA CAA CGG CTT GAC ACT

Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr

1325/361

GCA GAC CCT GCG ATG CTG TAT GCT GTG GTG GAT GGC GTG CCT CCG ACA CGC TGG AAG GAG

Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu

1385/381

TTC ATG CGG CTC CTG GGG CTG AGC GAG CAC GAG ATC GAG CGG CTG GAG CTG CAG AAC GGG

Phe Met Arg Leu Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly

1445/401

CGT TGC CTC CGC GAG GCT CAT TAC AGC ATG CTG GAA GCC TGG CGG CGC CGC ACA CCG CGA

Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg

1505/421

CAC GAG GCC ACG CTG GAC GTA GTG GGC CGC GTG CTT TGC GAC ATG AAC CTG CGT GGC TGC

His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met Asn Leu Arg Gly Cys

1565/441

CTG GAG AAC ATC CGC GAG ACT CTA GAA AGC CCT GCC CAC TCG TCC ACG ACC CAC CTC CCG

Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro

1625/461

CGA TAA

Arg Stop

1295/351

1355/371

1415/391

1475/411

1535/431

1595/451

GGCCACACCC CCACCTCAGG AACGGGACTC GAAGGACCAT CCTGCTAGAT 1680

GCCCTGCTTC CCTGTGAACC TCCTCTTTGG TCCTCTAGGG GGCAGGCTCG ATCTGGCAGG 1740

CTCGATCTGG CAGCCACTTC CTTGGTGCTA CCGACTTGGT GTACATAGCT TTTCCCAGCT 1800

GCCGAGGACA GCCTGTGCCA GCCACTTGTG CATGGCAGGG AAGTGTGCCA TCTGCTCCCA 1860

GACAGCTGAG GGTGCCAAAA GCCAGGAGAG GTGATTGTGG AGAAAAAGCA CAATCTATCT 1920

GATACCCACT TGGGATGCAA GGACCCAAAC AAAGCTTCTC AGGGCCTCCT CAGTTGATTT 1980

CTGGGGCCCTT TTCACAGTAG ATAAAACAGT CTTTGTATTG ATTATATCAC ACTAATGGAT 2040

GAACGGTTGA ACTCCCTAAG GTAGGGGGCAA GCACAGAACA GTGGGGTCTC CAGCTGGAGC 2100

CCCCGACTCT TGTAATACA CTAAAAATCT AAAAGTGAAA AAAAAAAAAA AAAAAAAAAA 2160

AAAAAAGGAA TTC

FIG. 9A

huTNF-R

GAATTCTCTG GACTGAGGCT CCAGTTCTGG CCTTTGGGGT TCAAGATCAC TGGGACCAGG 60
CCGTGATCTC TATGCCCCGAG TCTCAACCCT CAACTGTCAC CCCAAGGCAC TTGGGACGTC 120
CTGGACAGAC CGAGTCCCGG GAAGCCCCAG CACTGCCGCT GCCACACTGC CCTGAGCCCA 180
AATGGGGGAG TGAGAGGCCA TAGCTGTCTG GC

213/1	243/11
ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG	CTG CCA CTG GTG CTC CTG GAG CTG TTG GTG
Met Gly Leu Ser Thr Val Pro Asp Leu Leu	Leu Pro Leu Val Leu Leu Glu Leu Leu Val
273/21	303/31
GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG	GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA
Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu	Val Pro His Leu Gly Asp Arg Glu Lys Arg
333/41	363/51
GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC	CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC
Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile	His Pro Gln Asn Asn Ser Ile Cys Cys Thr
393/61	423/71
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT	GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn	Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
453/81	483/91
TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC	GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr	Ala Ser Glu Asn His Leu Arg His Cys Leu
513/101	543/111
AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT	CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC
Ser Cys Ser Lys Cys Arg Lys Glu Met Gly	Gln Val Glu Ile Ser Ser Cys Thr Val Asp
573/121	603/131
CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC	CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn	Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu
633/141	663/151
TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC	AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG
Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu	Asn Gly Thr Val His Leu Ser Cys Gln Glu
693/161	723/171
AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA	GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC
Lys Gln Asn Thr Val Cys Thr Cys His Ala	Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
753/181	783/191
TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG	TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG
Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu	Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
813/201	843/211
AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC	ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT
Asn Val Lys Gly Thr Glu Asp Ser Gly Thr	Thr Val Leu Leu Pro Leu Val Ile Phe Phe
873/221	903/231
GGT CTT TGC CTT TTA TCC CTC CTC TTC ATT	GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG
Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile	Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
933/241	963/251
TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA	TCG ACA CCT GAA AAA GAG GGG GAG CTT GAA
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys	Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu
993/261	1023/271
GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC	CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC
Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn	Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr
1053/281	1083/291
CCC ACC CTG GGC TTC AGT CCC GTG CCC AGT	TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC
Pro Thr Leu Gly Phe Ser Pro Val Pro Ser	Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
1113/301	1143/311
CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC	CGC AGA GAG GTG GCA CCA CCC TAT CAG GGG
Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro	Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
1173/321	1203/331
GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC	TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala	Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys

FIG. 9B

1233/341	1263/351	
TGG GAG GAC AGC GCC CAC AAG CCA CAG AGC	CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC	
Trp Glu Asp Ser Ala His Lys Pro Gln Ser	Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr	
1293/361	1323/371	
GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC	TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG	
Ala Val Val Glu Asn Val Pro Pro Leu Arg	Trp Lys Glu Phe Val Arg Arg Leu Gly Leu	
1353/381	1383/391	
AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG	CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA	
Ser Asp His Glu Ile Asp Arg Leu Glu Leu	Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln	
1413/401	1443/411	
TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC	ACG CCG CGG CGC GAG GCC ACG CTG GAG CTG	
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg	Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu	
1473/421	1503/431	
CTG GGA CGC GTG CTC CGC GAC ATG GAC CTG	CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG	
Leu Gly Arg Val Leu Arg Asp Met Asp Leu	Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala	
1533/441	1563/451	
CTT TGC GGC CCC GCC GCC CTC CCG CCC GCG	CCC AGT CTT CTC AGA TGA	1580
Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala	Pro Ser Leu Leu Arg Stop	

GGCTGCGCCC	CTGCGGGCAG	CTCTAAGGAC	CGTCCTGCGA	1620	
GATCGCCTTC	CAACCCCACT	TTTTTCTGGA	AAGGAGGGGT	CCTGCAGGGG	CAAGCAGGAG 1680
CTAGCAGCCG	CCTACTTGGT	GCTAACCCT	CGATGTACAT	AGCTTTTCTC	AGCTGCCTGC 1740
GCGCCGCCGA	CAGTCAGCGC	TGTGCGCGCG	GAGAGAGGTG	CGCCGTGGGC	TCAAGAGCCT 1800
GAGTGGGTGG	TTTGCGAGGA	TGAGGGACGC	TATGCCTCAT	GCCCGTTTGT	GGTGTCTCA 1860
CCAGCAAGGC	TGCTCGGGGG	CCCCTGGTTC	GTCCCTGAGC	CTTTTTCACA	GTGCATAAGC 1920
AGTTTTTTTT	GTTTTTGTTT	TGTTTTGTTT	TGTTTTTAAA	TCAATCATGT	TACACTAATA 1980
GAAACTTGGC	ACTCCTGTGC	CCTCTGCCTG	GACAAGCACA	TAGCAAGCTG	AACTGTCCTA 2040
AGGCAGGGGC	GAGCACGGAA	CAATGGGGCC	TTCAGCTGGA	GCTGTGGACT	TTTGTACATA 2100
CACTAAAATT	CTGAAGTTAA	AAAAAAAAAA	AAAAGGAATT	C	2141

FIG.10

